



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 123946

TO: Phillip Gabel
Location: 3e81 / 3c70
Wednesday, June 09, 2004
Art Unit: 1644
Phone: 272-0844
Serial Number: 09 / 891943

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1A51
Phone: 272-2504

jan.delaval@uspto.gov

Search Notes

Delaval, Jan

123946

From: Gabel, Phillip
Sent: Monday, June 07, 2004 9:23 AM
To: Delaval, Jan
Subject: 09/891,943 sequence search

jan

please perform a sequence and a sequence interference search for

09 / 891,943 (gallatin)

SEQ ID NO: 1

SEQ ID NO: 2

thanx

phillip gabel
art unit 1644
272-0844

1644 mailbox 3c70

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg Room Location: _____ Results Format Preferred (check): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples of relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with one appropriate serial number.

{

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher:	<i>Jen</i>	NA Sequence (#) <input checked="" type="checkbox"/>	STN _____
Searcher Phone #:	<i>22504</i>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location:		Structure (#) <input type="checkbox"/>	Questel/Orbit _____
Date Searcher Picked Up:	<i>6/17</i>	Bibliographic <input type="checkbox"/>	Dr.Link _____
Date Completed:	<i>6/19</i>	Litigation <input type="checkbox"/>	Lexis/Nexis _____
Searcher Prep & Review Time:		Fulltext <input type="checkbox"/>	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time:	<i>10</i>	Patent Family <input type="checkbox"/>	WWW/Internet _____
Online Time:	<i>+ 20</i>	Other <input type="checkbox"/>	Other (specify) _____

GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

```

BDM nucleic - nucleic search, using sw model
Run on: June 8, 2004, 05:52:06 ; Search time 22742 Seconds
          (without alignments)
          7101.229 Million cell updatd

Title: US-09-891-943-1
perfect score: 3726
Sequence: 1 tgacattcggactgtgtt.....agcataaaatttcataatgt

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

```

GenEmbL:*
 1: 9b_ba:*
 2: 9b_hhg:*
 3: 9b_in:*
 4: 9b_om:*
 5: 9b_oy:*
 6: 9b_pat:*
 7: 9b_ph:*
 8: 9b_pl:*
 9: 9b_pr:*
10: 9b_ro:*
11: 9b_sbs:*
12: 9b_sy:*
13: 9b_ur:*
14: 9b_v1:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_ir:*
19: em_mu:*
20: em_om:*
21: em_oz:*
22: em_oy:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sbs:*
28: em_un:*
29: em_v1:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pain:*
35: em_hg_rod:*
36: em_hg_mani:*

```

37: em_htgo_vrt: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

Pred. No. is the number of results predicted by chance to have a

```

US-09-891-943-1
June 8, 2004, 05:52:06 ; Search time 22742 Seconds
(w/o alignments)
7101.229 Million cell updates/sec

Title: US-09-891-943-1
perfect score: 3726
Sequence: 1 tgaccatccggactgtgtt.....agcataaaatccatatgt 3726

Scoring table: IDENTITY_NUC
Gapopen 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
  1: gb_ba;*
  2: gb_htg;*
  3: gb_in;*
  4: gb_om;*
  5: gb_ov;*
  6: gb_pac;*
  7: gb_ph;*
  8: gb_pl;*
  9: gb_pr;*
  10: gb_ro;*
  11: gb_st;*
  12: gb_sy;*
  13: gb_wnt;*
  14: gb_vii;*
  15: em_ba;*
  16: em_fun;*
  17: em_hum;*
  18: em_in;*
  19: em_m1;*
  20: em_om;*
  21: em_or;*
  22: em_ov;*
  23: em_wnt;*
  24: em_x;*
  25: em_y;*
  26: em_z;*
  27: em_ab;*
  28: em_ac;*
  29: em_ad;*
  30: em_af;*
  31: em_ag;*
  32: em_ah;*
  33: em_aj;*
  34: em_ao;*
  35: em_au;*
  36: em_ay;*
  37: em_au;*
  38: em_au;*
  39: em_au;*
  40: em_au;*
  41: em_au;*
  42: em_au;*
  43: em_au;*
  44: em_au;*
  45: em_au;*

```

RESULT	1	AR044695	AR044695	3726 bp
LOCUS			Sequence 1 from patent US 5817515.	
DEFINITION				
ACCESSION		AR044695	AR044695	AR044695
VERSION			1	1
KEYWORDS				GI:5966160
SOURCE			Unknown.	Unknown.
ORGANISM			Unclassified.	
REFERENCE			1 (bases 1 to 3726)	
AUTHORS			Gallatin, W. Michael. and Van der Vi	
TITLE			Human B2 integrin alpha subunit an	
JOURNAL			Patent: US 5817515-A 1 06-OCT-1998	
FEATURES			Location,Qualifiers	

RESULT 1
AR044695 AR044695
LOCUS LOCUS
ALIGNMENTS

Sequence 1 from patent US 5817515.
 DEFINITION AR044695
 ACCESSTION AR044695
 VERSION AR044695.1
 KEYWORDS SOURCE Unknown
 ORGANISM Unknown
 UNCLASSIFIED Unclassified.
 REFERENCE 1 (bases 1 to 3726)
 AUTHORS Gallatin,W.Michael I. and Van der Vieren,M.
 TITLE Human B2 integrin alpha subunit antibodies
 JOURNAL Patent : US 5817515-A 1 06-Oct-1998/
 FEATURES Location/Qualifiers

source	1. 3726	/organism="unknown"
	/mol_type="unassigned DNA"	
ORIGIN		
Query Match	100.0% ; Score 3726; DB 6; Length 3726;	
Best Local Similarity	100.0% ; Pred. No. 0;	
Matches 3722; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;		
Db	1 TGACCTTCGGAACTTCAGGAGGTTCTCGAGTCCTTCAGGATTCACCTGG 60	
Db	1 TGACCTTCGGAACTTCAGGAGGTTCTCGAGTCCTTCAGGATTCACCTGG 60	
Qy	1 AGTTCGGTGGATCTGACTCTGGTGGAGACCCCTGGCCAAACCGA 180	
Db	61 AGTTCGGTGGATCTGACTCTGGTGGAGACCCCTGGCCAAACCGA 120	
Db	61 AGTTCGGTGGAACTTCAGATCTTCAGGATTCACCTGGCCAAACCGA 120	
Qy	121 AGTTCGGTGGATCTGACTCTGGTGGAGACCCCTGGCCAAACCGA 180	
Db	121 AGTTCGGTGGATCTGACTCTGGTGGAGACCCCTGGCCAAACCGA 120	
Qy	181 CGGGAGGGCTTATGACTGCCCAGTCACGGCATTCGGTGCACA 240	
Db	181 CGGGAGGGCTTATGACTGCCCAGTCACGGCATTCGGTGCACA 240	
Db	181 CGGGAGGGCTTATGACTGCCCAGTCACGGCATTCGGTGCACA 240	
Qy	241 TCGCCCTGAGGGCTGAAACTATGTCCTTGGGCTGACCCCTGGAGCTCCACAGGGCT 300	
Db	241 TCGCCCTGAGGGCTGAAACTATGTCCTTGGGCTGACCCCTGGAGCTCCACAGGGCT 300	
Qy	301 CCCGGCTCTGCCCTGAGGGCTGACCCCTGGAGCTCCACAGGGCT 360	
Db	301 CCCGGCTCTGCCCTGAGGGCTGACCCCTGGAGCTCCACAGGGCT 360	
Qy	361 ACGGTTCTGCTCTGCCCTGGAGCTCCACAGGGCTGACCCCTGGAGCTCCACAGGGCT 420	
Db	361 ACGGTTCTGCTCTGCCCTGGAGCTCCACAGGGCTGACCCCTGGAGCTCCACAGGGCT 420	
Qy	481 TTGACCAAAATGACTTTAACAGATGAGGGTTGGCAAGCTGTCATGGCCCAAGTTG 540	
Db	481 TTGACCAAAATGACTTTAACAGATGAGGGTTGGCAAGCTGTCATGGCCCAAGTTG 540	
Qy	541 AGGGCACTGACACCCCTTTGACTGTGCACTTAACCTCTGAAGATCCACTTCA 600	
Db	541 AGGGCACTGACACCCCTTTGACTGTGCACTTAACCTCTGAAGATCCACTTCA 600	
Qy	601 CCTTCAACCAATTGGACCAAGCCGAGCAAGGCTGTGATCCATGTCAAC 660	
Db	601 CCTTCAACCAATTGGACCAAGCCGAGCAAGGCTGTGATCCATGTCAAC 660	
Qy	661 TGAAGAGCCCTGACGTTCTGGCAAGGCACTGAGTGTGACACGGTATTCATC 720	
Db	661 TGAAGAGCCCTGACGTTCTGGCAAGGCACTGAGTGTGACACGGTATTCATC 720	
Qy	781 ACTACAAAGACCCCTGGAAATACAGTATGCTTCAGGGCAAGGCTGGCATCA 840	
Db	781 ACTACAAAGACCCCTGGAAATACAGTATGCTTCAGGGCAAGGCTGGCATCA 840	
Qy	841 TCGCTAGCTATCGGGTGGACACGCTTCCAGGAACTGCAAGGGAGGTGA 900	
Db	841 TCGCTAGCTATCGGGTGGACACGCTTCCAGGAACTGCAAGGGAGGTGA 900	
Qy	901 ATACCATAGCTGCTGGCTCCAGGAACTGCTGGACACTTGGCAACGCC 960	
Db	901 ATACCATAGCTGCTGGCTCCAGGAACTGCTGGACACTTGGCAACGCC 960	
Qy	901 ATACCATAGCTGCTGGCTCCAGGAACTGCTGGACACTTGGCAACGCC 960	

Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cDNA/>
 Contact: am@bcm.tmc.edu
 Series: IRAK Plate: 30 Row: 9 Column: 12
 This clone was selected for full length sequence based on the following selection criteria: main criteria: frame This clone has the following problem: frame Location/Qualifiers
 1. 4056
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/10R"
 /clone="IRAK10090"
 /clone_type="mammary tumor metastasis"
 /tissue_type="arose spontaneously from a senescent (clonal) outgrowth infected with t1"
 /clone_id="NCI CGAP_Lu29"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"
 FEATURES
 Source
 Query Match 44.0%; Score 1638.8; DB 11;
 Best Local Similarity 68.0%; Prod. No. 0;
 Matches 2363; Conservative 0; Mismatches 1072;
 Matches 2363;
 Y 3 ACCTTCGGCAGCTGCTCTCTGAGTGTCTGGCTTCCTTA
 b 63 ACCGGATAGCCTTCCTTCATGGCTTGGGTCTTCCTTG
 Y 63 GGGAGAAGGCCAGATCTCCAGGAGATCAGGGCTT
 b 123 GAGAGAAGCTGACACATTTCACATGGAGCTGCTGAGTT
 Y 123 TTGGTGGATCTCACTCTGTTGGAGACCCCTGGAGGT
 b 183 TATGATAGTTCTGGGTGTTGGGACCAAGGGAAAT
 Y 183 GAGGGCTGTAATGCTGCGAGCTGCTCCACCGGATGCTGCA
 b 243 GGTGGCTCTACAATGTGGTATCACAGGCAACTTGA
 Y 243 CGGCTCTGGGCTGAACTGTCCTGGGCTGACCCCTGGC
 b 303 CCCCCAGGGCTGAACTGTCCTGGGCTGACAGACTGTGG
 Y 303 CGGCTCCAGCTGCTGGCCGGACCTGCAAGAGCTGTGG
 b 363 TGGCTGTTGGCTTGGCTTACTTGACACACATGGAC
 Y 363 GGTCTGCTGCTCTGGCTTGGGATCTGGGAGATCATCC
 b 423 GG - GGTGTTCTPACTGACTTCATTCAGAGGAGCC
 Y 423 CCAAGGTGTCCACATCAAGAATGGACATCTCTTCCTGAT
 b 481 CAGAGTGTCAAGGAGAACATGGTCTGTTCTGAT
 Y 483 GRCGAAATGACTTTAACCAAGATGAGGGCTTGTCTGAG
 b 541 AGTTCACATTTGAAATGCTGGACTTGTAAAGG
 Y 543 GGCAGCTGACACCCCTGGCTTGGACTGATGCAAGTAAACCC
 b 601 AGACCTGACACGGTTCTCCCTGATGCACTCTCTGAT
 Y 603 TTCAACCAATTGGACCCAGGAGCCAGGAGCTGGCTGG

661	Db	TTCAGAACATTCATCTCCAGCTCAAGGCCCTTAACTCTGTGAAAGCTCACTCTGTGAAAGCTTA 720
663	Qy	AAAGGGCTGAGGTTACGGCAAGGCCATCTGAGATGTTGACAGCTTCTGAACTGGGAG 722
721	Db	AGGGTACATACAGCTTCGCTTAAAGCTTACGGAACTGGGAG 780
723	Qy	AAGAAATGGGGCCGAAAGAAAGTCCCTATGTCATCACAGATGGGAGGAAG 782
781	Db	AAAGGGAGTGGATGCCCAAGGTCTTATGTCATCACAGATGGGAGGAAG 840
783	Qy	TACAAAGACCCCTGTTGAAATACAGTGTGATCCCGGAGAGAGGGCTGCAAGCTCATTC 842
841	Db	CGAGGAAACAATCTGGTTAGATAGCTGATCCCATGGAGGGCTGCAAGCTCATTC 900
843	Qy	CGCTTACGCTATCGGTTCCAGGGACCCACTGCGCCAGGAGCTGTGAAT 902
901	Db	CGTTATCAATGGGTTAGGAAGGGCTTACAAATCCAAAGCAGAATTAAG 960
903	Qy	ACCATAGCTCAGGCTCCAGGACCACTGGTCAAGCTTGCAGCCCTT 962
961	Db	GGCATTCATGCTTCCATGATACTTACGGTGGAGACTTGATGGTTTG 1020
963	Qy	GGGAGGATCCAAAGCAGCTGAGGAGAGCTTACAGTGTGAGCTTCCAGG 1022
1021	Db	AAGGATATTGAAATCTGTTGAGGAGAGATCTTGCATAGAGAACACCA 1080
1023	Qy	CCAGGAGCTCTTCAGCACAGAATCTCCCAAAGGCTTCAGAACAGCTCATG 1082
1081	Db	AGAGCAGTACTTTGATTGAGATGTCAGGCTCTGGAGCTTCAGTGTGTTAACCT 1140
1083	Qy	GATGGCCCTCTTCCTGGGGCTCTGGGAGCTTACCTGTTGAGCTCTGTAT 1142
1141	Db	GATGGACAGTTGGGGCTCTGGAGCTTCAGTGTGTTGAGCTCTGTAC 1200
1143	Qy	CCCCAAATAGGCCAACCTTCATCAACATGTCAGGGAC 1202
1201	Db	CCCTCAATATGAACTTCATCAACATGTCAGGGAC 1260
1203	Qy	TCTTAACCTGGGTACTTCACCGAGCTTGGGGTACAGAACCTGGCTCTG 1262
1261	Db	GCTTACCTGGTTACTCACCGGACTGCCCCTTGGAGGGCTCACGGCTGATCTG 1320
1263	Qy	GGGCCCCGGTACAGATACTGGGGCTTACCTGGGGTACAGAACCTGGCTCTG 1322
1321	Db	GGGCCCCCTGGCCACAGAACGGGCTTACCTGGGGCTTACAGGGAC 1380
1323	Qy	TGGGAGAAAGGGGAGTCAAGGGAGCTGGAGATGGCTCTACTTGGGGCTCTC 1382
1381	Db	TGGGGCCAAGTGTGAGTCAAGGGAGCTGGAGATGGCTCTACTTGGGGCTCT 1440
1383	Qy	TGCTCTGGATGTCAGCTGGAGCTGGAGCTGGAGCTGGCTCTACTTGGGGCTCT 1442
1441	Db	TGTTCTGTGACATGATAGAGCTGGAGCTGGAGCTGGAGCTGGGGCTCT 1500
1443	Qy	TACATGACAGACCCGAGGGGAGCTGGAGCTGGAGCTGGGGCTCT 1502
1501	Db	TACATGACACCCGAGGGGAGCTGGAGCTGGGGCTCT 1559
1560	-	-CAGCTGGATTGGGGCTTACCTGGGGCTTACCTGGGGCTCT 1562
1563	Qy	GGGGAGCCCTGAGGTGGGGCTTACCTGGGGCTTACCTGGGGCTCT 1622
1618	Db	GGGGGGCTGGCTGACGTGGCTAGGGAGCTGGGGCTTACCTGGGGCTCT 167
1623	Qy	GGGCCCCGGGAGACAGGAAGCCGGGGCTTACCTGGGGCTCT 1682
1678	Db	GTTGACCCGGAGAGGAGGAACGGGCTTACCTGGGGCTCT 1737
1683	Qy	TCCGGCATCGCCCCCTCCAGGGAGCTGGGGCTCT 1742

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM: nucleic - nucleic search, using sw model

Run on: June 8, 2004, 05:52:06 ; Search time 2021 Seconds
 (without alignments)
 7832.155 Million cell updates/sec

Title: US-09-891-943-1

Perfect score: 3726

Sequence: 1 tgaccttgcgtgtgtct.....agctaaaattttcatatgtct 3726

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: GeneSeq1980s:*
2: GeneSeq1990s:*
3: GeneSeq2000s:*
4: GeneSeqn2001as:*
5: GeneSeqn2001bs:*
6: GeneSeqn2002s:*
7: GeneSeqn2003as:*
8: GeneSeqn2003bs:*
9: GeneSeqn2003cs:*
```

No. is the number of results predicted by chance to have a score equal to or greater than the score of the result being printed, and is derived by analysis of the total score distribution.

MAPTES

Result No.	Score	Query	Match	Length	DB	ID
1	3726	100.0	3726	2	AAQ1712	
2	3726	100.0	3726	2	AAV9220	
3	3726	100.0	3726	2	AAV1540	
4	3726	100.0	3726	2	AAV5236	
5	3726	100.0	3726	2	AAV5281	
6	3726	100.0	3726	2	AAV0453	
7	3726	100.0	3726	6	AAV6014	
8	3726	100.0	3726	6	ABK82404	
9	3699	99.3	3785	2	AAT79275	
10	3699	99.3	3785	2	AAT53116	
11	3699	99.3	3785	2	AAT67299	
12	3699	99.3	3785	2	AAV0458	
13	3699	99.3	3785	6	AAV60094	
14	3699	99.3	3785	6	ABK82484	
15	3583	96.2	3956	2	AAT7274	
16	3583	96.2	3956	2	AAV35115	
17	3583	96.2	3956	2	AAV67298	
18	3583	96.2	3956	2	AAV08457	
19	3583	96.2	3956	3	AAV60093	
20	3583	96.2	3956	6	ABK82483	
21	2315.2	62.1	3803	2	AAT79256	
22	2315.2	62.1	3803	2	AAT15175	
23	2315.2	62.1	3803	2	AAV52123	

ALIGNMENTS

RESULT 1
 AAQ91712 AAQ91712 standard; cDNA; 3726 BP.
 ID AAQ91712
 XX
 AAQ91712;
 AC
 XX DT 28-DBC-1995 (first entry)
 XX DE Human beta-2 integrin alpha-d cDNA.
 XX KW Beta-2 integrin alpha-d subunit; antiinflammatory; arteriosclerosis;
 KW inflammatory bowel disease; asthma; ss.

Location/Qualifiers	Attribute	Value
3 . .3488	Key	XX
	CDS	FH
		FT
		FT

PN WO9517412-A1.
 XX
 PD 29-JUN-1995.
 XX
 PT 21-DEC-1994; 94WO-US014832.
 XX PR 23-DEC-1993; 94US-00173447.
 PR 05-AUG-1994; 94US-00286889.
 XX
 PA (ICCS-) ICOS CORP.
 XX PI Gallatin WM, Van Der Vieren M;
 XX DR WPI-1995-240603/31.
 DR P-PDB; AAR7166.
 XX PT Alpha sub-unit polypeptide of human beta 2 integrin - used to identify
 PT potential antiinflammatory agents, for the treatment of graft
 PT arteriosclerosis, inflammatory bowel disease, asthma, etc.
 XX
 PS Claim 1; Page 82-87; 172PP; English.
 XX
 CC A probe based on a partial cDNA clone (given in AAQ91727) of canine alpha
 CC -TM1 was used to screen a human spleen cDNA library to identify clone
 CC 19A2 encoding the beta-1 integrin alpha-subunit, alpha-d. The cDNA was
 CC manipulated to allow expression of recombinant alpha-d subunit in COS and
 CC CHO cells

XX	SQ	Sequence	3726 BP; 817 A; 1064 C; 1054 G; 791 T; 0 U; 0 Other;
	Query	Match	100.0%;
	Best	Local Similarity	100 %;
	Matches	3726;	Conservative 0;
	Db	Indels	0;
	Db	Gaps	0;
Qy	1	TGACCTTCGGCACTTGCTTCTCTGAAGTCCTGCTGCTTCCTTCTTCAACTCTGG	60
Db	1	TGACCTTCGGCACTTGCTTCTCTGAAGTCCTGCTGCTTCCTTCTTCAACTCTGG	60
Qy	61	ATGTGAGGGCCCTAAGCTTCTCAGAGGATGCCAGGGCTTGGCCAGAGCTGGC	120
Db	61	ATGTGAGGGCCCTAAGCTTCTCAGAGGATGCCAGGGCTTGGCCAGAGCTGGC	120
Qy	121	AGTTCGGTGGATCTCAACTCTGGGGAGACCCCTGAGGTGGGGCCACACAGA	180
Db	121	AGTTCGGTGGATCTCAACTCTGGGGAGACCCCTGAGGTGGGGCCACACAGA	180
Qy	181	CGGAACTGGCTGTATGACTGCGCACTGGCTCCACGGGATCTGGCTGACAA	240
Db	181	CGGAACTGGCTGTATGACTGCGCACTGGCTCCACGGGATCTGGCTGACAA	240
Qy	241	TCGGCCCTGAGGCCGTTGAAACATGTCCTTGGACCCCTGAGCTTCAACAGGCT	300
Db	241	TCGGCCCTGAGGCCGTTGAAACATGTCCTTGGCTGAGCCCTGAGCTTCAACAGGCT	300
Qy	301	CCGGGTCCTGGCTGCCGACCTGGCCGACCTGGCAAGAGCTCTGGGGAGAAC	360
Db	301	CCGGGTCCTGGCTGCCGACCTGGCCGACCTGGCAAGAGCTCTGGGGAGAAC	360
Qy	361	AGGGTCTGCTCCGCTGGCTGGCTGGGAGATCATCGAGTCTCCGAGGCCA	420
Db	361	AGGGTCTGCTCCGCTGGCTGGCTGGGAGATCATCGAGTCTCCGAGGCCA	420
Qy	421	CGCCAGAGTGTCCACATCAAGAGATGGACATGCTTCTCTGATGGGGCTGTGAGCA	480
Db	421	CGCCAGAGTGTCCACATCAAGAGATGGACATGCTTCTCTGATGGGGCTGTGAGCA	480
Qy	481	TTGACCAAATGACTTTAACCGATGAGGGCTTGTCCAACCTGTCATGGCCAGTTG	540
Db	481	TTGACCAAATGACTTTAACCGATGAGGGCTTGTCCAACCTGTCATGGCCAGTTG	540
Qy	541	AGGGCACTGACACCCATTGGCACTGATGCAAGCTAAACCTCTGAAGATCCATICA	600
Db	541	AGGGCACTGACACCCATTGGCACTGATGCAAGCTAAACCTCTGAAGATCCATICA	600
Qy	601	CCCTCAACCAATTGGCAACGGCCAGGGCACTGATGCAAGCTAACTGGTCAAC	660
Db	601	CCCTCAACCAATTGGCAACGGCCAGGGCACTGATGCAAGCTAACTGGTCAAC	660
Qy	661	TGAAGGGCTGACGTTCAAGGGCAAGGGCATCTGACAGTGGTAACAGTTTATC	720
Db	661	TGAAGGGCTGACGTTCAAGGGCAAGGGCATCTGACAGTGGTAACAGTTTATC	720
Qy	721	ATAGAAATGGGGCCGAAAATGGCTGACAGGATCTCATCGATGGGAGA	780
Db	721	ATAGAAATGGGGCCGAAAATGGCTGACAGGATCTCATCGATGGGAGA	780
Qy	781	ACTACAAAGACCCCTGGAAATACAGTGTATGTCATCCTCCAGGGAGAGA	840
Db	781	ACTACAAAGACCCCTGGAAATACAGTGTATGTCATCCTCCAGGGAGAGA	840
Qy	841	TCGGCTAGCTATGGGTGGCAACGGTTTCAAGGGACCCACTGGCAAGGAGCTGA	900
Db	841	TCGGCTAGCTATGGGTGGCAACGGTTTCAAGGGACCCACTGGCAAGGAGCTGA	900
Qy	901	ATACCATGCTGCTGGCTGGCAAGGACCACTGGCTGGCAACCTGGCAAGGAGCTGA	960
Db	901	ATACCATGCTGCTGGCTGGCAAGGACCACTGGCTGGCAACCTGGCAAGGAGCTGA	960
Qy	961	TGGCACTGGATCCAGAAGGAGCTGAGGAAGATCTATGCAAGTGGGAAACCA	1020

Ddb	961	TTCGGAGATCCAGAACAGCTGCAAGGAGAATCTATGCACTTGGGGAA;CCCTGTC	1020
Qy	1021	GGCAAGGAGCTTCCAGAACAGCTGCAAGGAGAATCTATGCACTTGGGGAA;CCCTGTC	1080
Db	1021	GGCAAGGAGCTTCCAGAACAGCTGCAAGGAGAATCTATGCACTTGGGGAA;CCCTGTC	1080
Qy	1081	TGATGGCTCTCTGGGGAGTTACCTGGCTGAGGTCTGGCTTCTGT	1140
Db	1081	TGATGGCTCTCTGGGGAGTTACCTGGCTGAGGTCTGGCTTCTGT	1140
Qy	1141	ATCCCCAAATAAGGCCAACCTATCAAATGTTCAAGGAAATGGACATGGGG	1200
Db	1141	ATCCCCAAATAAGGCCAACCTATCAAATGTTCAAGGAAATGGACATGGGG	1200
Qy	1201	ACCTTACCTGGGTTACCTCCAGGAGCTGAGCCCTGGAAAGGGTACAGAACACTGGTC	1260
Db	1201	ACCTTACCTGGGTTACCTCCAGGAGCTGAGCCCTGGAAAGGGTACAGAACACTGGTC	1260
Qy	1261	TGGGGCCCCCGTATCCAGCATCCGGAAAGCTGATCCTGCTACTTGGGTCT	1320
Db	1261	TGGGGCCCCCGTATCCAGCATCCGGAAAGCTGATCCTGCTACTTGGGTCT	1320
Qy	1321	AAATGGGAGAGAGGGCGAAGCTGCACTGGGAACTGGGTCT	1380
Db	1321	AAATGGGAGAGAGGGCGAAGCTGCACTGGGAACTGGGTCT	1380
Qy	1381	TCTGTCCTGGATGTGGAGCCATGGAGCACTGATCCTCATGGGGCCCC	1440
Db	1381	TCTGTCCTGGATGTGGAGCCATGGAGCACTGATCCTCATGGGGCCCC	1440
Qy	1441	ATTACATGAGAACCCAGGGCAAGGAGCTGAGGGCCACACCTGGCGT	1500
Db	1441	ATTACATGAGAACCCAGGGCAAGGAGCTGAGGGCCACACCTGGCGT	1500
Qy	1501	GGGTGCACTGGCACTGGCTGAGCTGGCTGTTCTGGGTGAGGGCC	1560
Db	1501	GGGTGCACTGGCACTGGCTGAGCTGGCTGTTCTGGGTGAGGGCC	1560
Qy	1561	TTGGGGAGGCCCTGAGCTGGGATGCTGATGAGCTGATAGCTGGCCA	1620
Db	1561	TTGGGGAGGCCCTGAGCTGGGATGCTGATGAGCTGATAGCTGGCCA	1620
Qy	1621	TTGGGGCCCCGGAGAGCACTGGGAGCTGGCTGAGCTGGCTGAGCTGGCCA	1680
Db	1621	TTGGGGCCCCGGAGAGCACTGGGAGCTGGCTGAGCTGGCTGAGCTGGCCA	1680
Qy	1681	AAATCCGGCATGGCCCTCCACAGCAGCGGATTTGGCACTCCAGCTGGC	1740
Db	1681	AAATCCGGCATGGCCCTCCACAGCAGCGGATTTGGCACTCCAGCTGGC	1740
Qy	1741	TGCACTTGGCACTGGGAGCTGAGCTGGGCTGAGGACCTCACCAGGATGGACTGTGG	1800
Db	1741	TGCACTTGGCACTGGGAGCTGAGCTGGGCTGAGGACCTCACCAGGATGGACTGTGG	1800
Qy	1801	ACCTGGCCCTGGGCCCCGGCCAGCTGGCTGCTCCAGGAGCTGGGTGTGG	1860
Db	1801	ACCTGGCCCTGGGCCCCGGCCAGCTGGCTGCTCCAGGAGCTGGGTGTGG	1860
Qy	1861	TGGGGTGGCATGAGATTCAGCCCTGGAGGGTGGCCAGGCTGTGCTGGG	1920
Db	1861	TGGGGTGGCATGAGATTCAGCCCTGGAGGGTGGCCAGGCTGTGCTGGG	1920
Qy	1921	AAGAGAGCCAGCTGGTACATCAAGGCTGTTGAGGTGGACATCGGACTG	1980
Db	1921	AAGAGAGCCAGCTGGTACATCAAGGCTGTTGAGGTGGACATCGGACTG	1980
Qy	1981	GCTCACTGGACCAGCTGGTACATCAAGGCTGTTGAGGTGGACATCGGACTG	2040
Db	1981	GCTCACTGGACCAGCTGGTACATCAAGGCTGTTGAGGTGGACATCGGACTG	2040
Qy	2041	CAGGTGCTGCACTCTCGTGGCCATTTCATGAAACCAAGAACCCACTTGTGCTGGAA	2100
Db	2041	CAGGTGCTGCACTCTCGTGGCCATTTCATGAAACCAAGAACCCACTTGTGCTGGAA	2100

OM nucleic - nucleic search, using SW model

Run on: June 8, 2004, 16:01:04 ; Search time 4734 Seconds
(without alignments)

3590.620 Million cell updates/sec

Title: US-09-891-943-1

Perfect score: 3726

Scoring table: IDENTITY_NUC

GAPOP 10_0 , Gapext 1.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Published_Application_NA:*

1: /cgn2_6_ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6_ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6_ptodata/2/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6_ptodata/2/pubpna/US05_PUBCOMB.seq:*

5: /cgn2_6_ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6_ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6_ptodata/2/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6_ptodata/2/pubpna/US09_PUBCOMB.seq:*

9: /cgn2_6_ptodata/2/pubpna/US09B_PUBCOMB.seq:*

10: /cgn2_6_ptodata/2/pubpna/US09C_PUBCOMB.seq:*

11: /cgn2_6_ptodata/2/pubpna/US09_N_PUB.seq:*

12: /cgn2_6_ptodata/2/pubpna/US09_N_PUB.seq:*

13: /cgn2_6_ptodata/2/pubpna/US09_N_PUB.seq:*

14: /cgn2_6_ptodata/2/pubpna/US10_PUBCOMB.seq:*

15: /cgn2_6_ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6_ptodata/2/pubpna/US10C_PUBCOMB.seq:*

17: /cgn2_6_ptodata/2/pubpna/US10_N_PUB.seq:*

18: /cgn2_6_ptodata/2/pubpna/US10_N_PUB.seq:*

19: /cgn2_6_ptodata/2/pubpna/US10_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query ID	Match ID	Length	DB ID	Description
1	3726	100.0	3726	9	US-09-350-239-1
2	3726	100.0	3726	10	US-09-891-943-1
3	3699	99.3	3785	9	US-09-350-239-98
4	3699	99.3	3785	10	US-09-891-943-98
5	3583	96.2	3956	9	US-09-150-251-97
6	3583	96.2	3956	10	US-09-891-943-97
7	2315.2	62.1	3803	9	US-09-350-239-52
8	2315.2	62.1	3803	10	US-09-891-943-52
9	2304.2	61.8	3597	9	US-09-350-251-54
10	2304.2	61.8	3597	10	US-09-891-943-54
11	2300.2	61.7	3528	9	US-09-350-251-36
12	2300.2	61.7	3228	10	US-09-891-943-36
13	2210.8	59.3	3519	9	US-09-350-251-45
14	2210.8	59.3	3519	10	US-09-891-943-45

Qy

ALIGNMENTS

RESULT 1	US-09-350-259-1	; Sequence 1, Application US/09350259
		; Patent No. US20020062005A1
		; GENERAL INFORMATION:
		; APPLICANT: Gallatin, Michael W.
		; APPLICANT: Van der Vieren, Monica
		; TITLE OF INVENTION: No. US20020062005A1 Human 2
		; FILE REFERENCE: 7866/7504
		; CURRENT FILING DATE: 1999-07-08
		; EARLIER APPLICATION NUMBER: 09/193,043
		; EARLIER FILING DATE: 1998-11-16
		; EARLIER APPLICATION NUMBER: 08/173,497
		; EARLIER FILING DATE: 1993-12-23
		; EARLIER APPLICATION NUMBER: 08/286,889
		; EARLIER FILING DATE: 1994-08-05
		; EARLIER APPLICATION NUMBER: 08/362,652
		; EARLIER FILING DATE: 1994-12-1
		; EARLIER APPLICATION NUMBER: 08/943,363
		; EARLIER FILING DATE: 1997-10-03
		; NUMBER OF SEQ ID NOS: 114
		; SOFTWARE: Patentin Ver. 2.0
		; SEQ ID NO 1
		; LENGTH: 3726
		; TYPE: DNA
		; ORGANISM: Homo sapiens
		; FEATURE:
		; NAME/KEY: CDS
		; LOCATION: (3) . (3485)
		; US-09-350-259-1
		Query Match 100.0% Score 3726; DB 9; Length 3726;
		Best Local Similarity 100.0% Pred. No. 0;
		Matches 3726; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
		Sequence 36, App1
		Sequence 36, App1
		Sequence 45, App1
		Sequence 45, App1

Qy

1

TGACCTTCGGCACTGTGCTTCCTGTAGTGGATCAACCTGG 60

	1	TGACTCTGGCACTGCTCTTCTGAGTGTCTGGCTTCTGAGTGTCTGGAGAAGCTTCACTGGATCAACCTGG	60	Db
Db	61	ATGGGAGGAGCTTCAATCTTCCAGGAGATGAGCAGGCTTGGAGAAGCTGGTC	120	Qy
Qy	61	ATGGGAGGAGCTTCAATCTTCCAGGAGATGAGCAGGCTTGGAGAAGCTGGTC	120	Db
Db	121	AGTCGGTGGACTCTTCAGGTTGAGCTGGAGGACCCGAGGAACTCCAGA	180	Qy
Qy	121	AGTCGGTGGACTCTTCAGGTTGAGCTGGAGGACCCGAGGAACTCCAGA	180	Db
Db	181	CGGACGCTTGTATGATGCTGGAGGAGCTGGAGGACCCGAGGAACTCCAGA	240	Qy
Qy	181	CGGACGCTTGTATGATGCTGGAGGAGCTGGAGGACCCGAGGAACTCCAGA	240	Db
Db	241	TCGGCCCTGAGGCCGTTAACAGTCTGGCTGAGCCTCCACCAACGGGT	300	Qy
Qy	241	TCGGCCCTGAGGCCGTTAACAGTCTGGCTGAGCCTCCACCAACGGGT	300	Db
Db	241	TGCGCCCTGAGGCCGTTAACAGTCTGGCTGAGCCTCCACCAACGGGT	300	Qy
Qy	301	CCGGGTCCTGGCTTCTGGCTGGGGCTGGGGAGAAGCTCATCTCAA	360	Db
Db	301	CCGGGTCCTGGCTTCTGGCTGGGGCTGGGGAGAAGCTCATCTCAA	360	Qy
Qy	361	AGGGTCTGGCTTCTGGCTGGGGCTGGGGAGAAGCTCATCTCAA	420	Db
Db	361	AGGGTCTGGCTTCTGGCTGGGGCTGGGGAGAAGCTCATCTCAA	420	Qy
Qy	421	CGCAGAGTGTCCACATCAAGAGATGGACATCTGGCTGGAGATCA	480	Db
Db	421	CGCAGAGTGTCCACATCAAGAGATGGACATCTGGCTGGAGATCA	480	Qy
Qy	481	TTCACCAAAATGACTTTAACAGAGATGGAGGGCTTGTCAAGCTGGCTGAGTTTG	540	Db
Db	481	TTCACCAAAATGACTTTAACAGAGATGGAGGGCTTGTCAAGCTGGCTGAGTTTG	540	Qy
Qy	541	AGGGCACTCAACOCTGTTGACTGTGCAATRACTAACCTCTGAAAGATCCACTTCA	600	Db
Db	541	AGGGCACTCAACOCTGTTGACTGTGCAATRACTAACCTCTGAAAGATCCACTTCA	600	Qy
Qy	601	CCPTCACCAATTCCGGCAAGCCGGAGCCAGAGCCTGGATCCCATCGTCCAAC	660	Db
Db	601	CCPTCACCAATTCCGGCAAGCCGGAGCCAGAGCCTGGATCCCATCGTCCAAC	660	Qy
Qy	661	TGAAAGGCTTCAAGTCCAGTGTGCAAGTGTGCAAGCTTCACTTCATC	720	Db
Db	661	TGAAAGGCTTCAAGTCCAGTGTGCAAGTGTGCAAGCTTCACTTCATC	720	Qy
Qy	721	ATAGAAATGGGCCGAAAGATGCCAACAGAACATCTCATCATGAGCCAGA	780	Db
Db	721	ATAGAAATGGGCCGAAAGATGCCAACAGAACATCTCATCATGAGCCAGA	780	Qy
Qy	781	AGTACAAAGACCCCTGGATACTGTGATGCTTCCCAAGGAGGCTGGATCA	840	Db
Db	781	AGTACAAAGACCCCTGGATACTGTGATGCTTCCCAAGGAGGCTGGATCA	840	Qy
Qy	841	TCCCTACTGCTTGGGGGGAGACGCTTCAAGGAGCCACTGGAGGTGA	900	Db
Db	841	TCCCTACTGCTTGGGGGGAGACGCTTCAAGGAGCCACTGGAGGTGA	900	Qy
Qy	901	ATACCATGACTGGCTTCCGGAGAACAGCTGGTCAAGCTGGTCAACTTGGAGCC	960	Db
Db	901	ATACCATGACTGGCTTCCGGAGAACAGCTGGTCAAGCTGGTCAACTTGGAGCC	960	Qy
Qy	961	TTGGAGCATCCAGAGCAGCTGGAGAACAGCTGGTCAAGCTGGTCAACTTGGAGCC	1020	Db
Db	961	TTGGAGCATCCAGAGCAGCTGGAGAACAGCTGGTCAAGCTGGTCAACTTGGAGCC	1020	Qy
Qy	1021	GGCGAGAACCTCCAGGAGAACAGCTGGAGAACAGCTGGTCAAGCTGGTCAACTTGGAGCC	1080	Db
Db	1021	GGCGAGAACCTCCAGGAGAACAGCTGGAGAACAGCTGGTCAAGCTGGTCAACTTGGAGCC	1080	Qy
Qy	1081	TGATGGCTTCTGCTGGGGAGCTTAACTGCTGGAGGCTTAACTGCTGG	1140	Db

GenCore version 5.1.6
 Copyright (C) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
 Run on: June 8, 2004, 05:52:06 ; Search time 282 Seconds
 (without alignments)
 7332.436 Million cell updates/sec

Title: US-09-891-943-1
 Perfect score: 3726

Sequence: 1 tgaccttcggactgttgttt.....agcataaaatttcatatgt 3726

Scoring table: IDENTITY_NUC
 Gapopen 10.0 , Gapext 1.0

Searched:

Total number of hits satisfying chosen parameters:

1365418

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : Issued Patents N/A
 1: /cgn2_6/prodata/2/ina/5A_COMB.seq:
 2: /cgn2_6/prodata/2/ina/5B_COMB.seq:
 3: /cgn2_6/prodata/2/ina/5A_COMB.seq:
 4: /cgn2_6/prodata/2/ina/6B_COMB.seq:
 5: /cgn2_6/prodata/2/ina/PECTUS_COMB.seq:
 6: /cgn2_6/prodata/2/ina/backfiles.seq:
 7: /cgn2_6/prodata/2/ina/backfiles.seq:
 8: /cgn2_6/prodata/2/ina/backfiles.seq:
 9: /cgn2_6/prodata/2/ina/backfiles.seq:
 10: /cgn2_6/prodata/2/ina/backfiles.seq:
 11: /cgn2_6/prodata/2/ina/backfiles.seq:
 12: /cgn2_6/prodata/2/ina/backfiles.seq:
 13: /cgn2_6/prodata/2/ina/backfiles.seq:
 14: /cgn2_6/prodata/2/ina/backfiles.seq:
 15: /cgn2_6/prodata/2/ina/backfiles.seq:
 16: /cgn2_6/prodata/2/ina/backfiles.seq:
 17: /cgn2_6/prodata/2/ina/backfiles.seq:
 18: /cgn2_6/prodata/2/ina/backfiles.seq:
 19: /cgn2_6/prodata/2/ina/backfiles.seq:
 20: /cgn2_6/prodata/2/ina/backfiles.seq:
 21: /cgn2_6/prodata/2/ina/backfiles.seq:
 22: /cgn2_6/prodata/2/ina/backfiles.seq:
 23: /cgn2_6/prodata/2/ina/backfiles.seq:
 24: /cgn2_6/prodata/2/ina/backfiles.seq:
 25: /cgn2_6/prodata/2/ina/backfiles.seq:
 26: /cgn2_6/prodata/2/ina/backfiles.seq:
 27: /cgn2_6/prodata/2/ina/backfiles.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3726	100.0	3726	1	US-08-173-497-1 Sequence 1, Appli Sequence 1, Appli
2	3726	100.0	3726	1	US-08-185-678-1 Sequence 1, Appli Sequence 1, Appli
3	3726	100.0	3726	1	US-08-185-678-1 Sequence 1, Appli Sequence 1, Appli
4	3726	100.0	3726	1	US-08-185-678-1 Sequence 1, Appli Sequence 1, Appli
5	3726	100.0	3726	1	US-08-185-678-1 Sequence 1, Appli Sequence 1, Appli
6	3726	100.0	3726	2	US-08-182-291A-1 Sequence 1, Appli Sequence 1, Appli
7	3726	100.0	3726	2	US-08-194-363-1 Sequence 1, Appli Sequence 1, Appli
8	3726	100.0	3726	3	US-08-193-041-1 Sequence 1, Appli Sequence 1, Appli
9	3726	100.0	3726	4	US-09-688-307A-1 Sequence 1, Appli Sequence 1, Appli
10	3726	100.0	3726	4	US-09-310-259-1 Sequence 1, Appli Sequence 1, Appli
11	3699	99.3	3785	1	US-08-185-618-98 Sequence 98, Appli Sequence 98, Appli
12	3699	99.3	3785	1	US-08-165-672-98 Sequence 98, Appli Sequence 98, Appli
13	3583	96.2	3785	2	US-08-182-291A-98 Sequence 97, Appli Sequence 97, Appli
14	3699	99.3	3785	2	US-08-193-363-98 Sequence 98, Appli Sequence 98, Appli
15	3699	99.3	3785	3	US-09-193-041-98 Sequence 98, Appli Sequence 98, Appli
16	3699	99.3	3785	4	US-09-688-307A-98 Sequence 98, Appli Sequence 98, Appli
17	3699	99.3	3785	4	US-09-310-259-98 Sequence 97, Appli Sequence 97, Appli
18	3583	96.2	3956	1	US-08-145-618-97 Sequence 97, Appli Sequence 97, Appli
19	3583	96.2	3956	1	US-08-605-671-97 Sequence 97, Appli Sequence 97, Appli
20	3583	96.2	3956	2	US-08-482-291A-97 Sequence 97, Appli Sequence 97, Appli
21	3583	96.2	3956	2	US-08-943-363-97 Sequence 97, Appli Sequence 97, Appli
22	3583	96.2	3956	3	US-09-193-043-97 Sequence 97, Appli Sequence 97, Appli
23	3583	96.2	3956	4	US-09-688-307A-97 Sequence 97, Appli Sequence 97, Appli
24	3583	96.2	3956	4	US-09-310-259-97 Sequence 52, Appli Sequence 52, Appli
25	2315.2	62.1	3803	1	US-08-485-618-52 Sequence 52, Appli Sequence 52, Appli
26	2315.2	62.1	3803	1	US-08-362-652-52 Sequence 52, Appli Sequence 52, Appli
27	2315.2	62.1	3803	1	US-08-605-672-52 Sequence 52, Appli Sequence 52, Appli

ALIGNMENTS

RESULT 1
 US-08-173-497-1
 ; Sequence 1, Application US/08173497
 ; Patent No. 5477958
 ; GENERAL INFORMATION:
 ; APPLICANT: Galatin, W. Michael
 ; TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 S. Wacker Drive, 6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/173,497
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5437958and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 27866/31363
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-774-6300
 ; TELEFAX: 312-474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3726 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 3..3495
 ; US-08-173-497-1

Query Match 100.0%; Score 3726; DB 1; Length 3726;
 Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;
 Matches 3726; Conservative 0; Mismatches 0;

QY	1	TGACCTTGGCACTGGTCTCTGACTGCTCTGTTTATCGGAITCAACCTGG	60	
Db	1	TGACCTTGGCACTGGTCTCTGACTGCTCTGTTTATCGGAITCAACCTGG	60	
QY	61	ATGGAAAGAGCTAACGATCTTCCAGAAGGATGCAAGGGCTTGGCAAGGG	120	
Db	61	ATGGAAAGAGCTAACGATCTTCCAGAAGGATGCAAGGGCTTGGCAAGGG	120	
QY	121	AGTTCGGTGGATCTCGACTCTGGTGGAGCACCCCTCGAAGTGGCGCCAA	180	
Db	121	AGTTCGGTGGATCTCGACTCTGGTGGAGCACCCCTCGAAGTGGCGCCAA	180	
QY	181	CGGAACGGCTTACGATCTGGTGGAGCACCCCTCGAAGTGGCGCCAA	240	
Db	181	CGGAACGGCTTACGATCTGGTGGAGCACCCCTCGAAGTGGCGCCAA	240	
QY	241	TCCGCCCTGGAGCCCTGGCTGAACCTGGCAGCGCTCACCAAAGGCT	300	
Db	241	TCCGCCCTGGAGCCCTGGCTGAACCTGGCAGCGCTCACCAAAGGCT	300	
QY	301	CCGGCGCTGGCCCTGGCTGGCGCTGGAGAACATCATCTCAA	360	
Db	301	CCGGCGCTGGCCCTGGCTGGCGCTGGAGAACATCATCTCAA	360	
QY	361	AGGTTCTCCCTCTGGCTGGCGCTGGAGAACATCCAGAACGGCA	420	
Db	361	AGGTTCTCCCTCTGGCTGGCGCTGGAGAACATCCAGAACGGCA	420	
QY	421	CGCCAGAGGTCCACATCAAGATGGAACTCTCTCTGGCTGTTGGAGCA	480	
Db	421	CGCCAGAGGTCCACATCAAGATGGAACTCTCTCTGGCTGTTGGAGCA	480	
QY	481	TTGACCAAAATGACTTAACTGGAGGGCTTGTCTCAAGTGGCCAGTTG	540	
Db	481	TTGACCAAAATGACTTAACTGGAGGGCTTGTCTCAAGTGGCCAGTTG	540	
QY	541	AGGCACTAACACCTCTGACTGACTCGAACCTCTGATGAACTTC	600	
Db	541	AGGCACTAACACCTCTGACTGACTCGAACCTCTGATGAACTTC	600	
QY	601	CCTTCACCCAAATTGGACACGCCGAGCCAGGAGCTGGGATCCATGTC	660	
Db	601	CCTTCACCCAAATTGGACACGCCGAGCCAGGAGCTGGGATCCATGTC	660	
QY	661	TGAAGGGCTGACGTTCAAGGCCGAGGATCTGAGTCACTTCATC	720	
Db	661	TGAAGGGCTGACGTTCAAGGCCGAGGATCTGAGTCACTTCATC	720	
QY	721	ATAAGAAATGGCCGAAAGTCCAAAGAAGATCCTCATAGTGGCGA	780	
Db	721	ATAAGAAATGGCCGAAAGTCCAAAGAAGATCCTCATAGTGGCGA	780	
QY	781	AGTACAAAGAACCCCTGGATACTGGTGTGATCTGGAGAAGGTGCTCA	840	
Db	781	AGTACAAAGAACCCCTGGATACTGGTGTGATCTGGAGAAGGTGCTCA	840	
QY	841	TCCGCTACCTATGGGCTGGAGACGCTTCCAGGACGCCACTGCG	900	
Db	841	TCCGCTACCTATGGGCTGGAGACGCTTCCAGGACGCCACTGCG	900	
QY	901	ATACATCAGCTAGGAGCTGGAGAAGATCTACAGTGGTCACTG	960	
Db	901	ATACATCAGCTAGGAGCTGGAGAAGATCTACAGTGGTCACTG	960	
QY	961	TTGGCAGCATCCAGAGGACTGAGGAGAAGATCTACAGTGGAA	1020	
Db	961	TTGGCAGCATCCAGAGGACTGAGGAGAAGATCTACAGTGGAA	1020	
QY	1021	GGCAAGGAGCTTCCAGGACGAGATGCTCCAGAGGCTCACAA	1080	
Db	1021	GGCAAGGAGCTTCCAGGACGAGATGCTCCAGAGGCTCACAA	1080	
QY	1021	TGGAGGATCTGGTACCCCCATCATCTGACCTCAACTCTGACCTCA	1140	
Db	1021	TGGAGGATCTGGTACCCCCATCATCTGACCTCAACTCTGACCTCA	1140	

Gencore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2004, 09:36:53 ; Search time 27 Seconds
(without alignments)
4136.236 Million cell updates/sec

Title: US-09-891-943-2
Perfect Score: 5987
Sequence: 1 TFGTVLILLSVLASYHGFNLD.....DTATFSGDDFSCTVAPNVPPLS 1161

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : PIR_78;*
1: Pir1;*
2: Pir2;*
3: Pir3;*
4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the result being printed.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	3818	63.8	1163	1 PWHUIC	cell surface Glyco
2	3455	52.7	1153	1 PWHUIC	cell surface Glyco
3	3327	55.6	1153	2 S00551	leukocyte surface
4	1474	24.6	1170	2 S03308	cell surface Glyco
5	1457.5	24.3	1163	2 156126	lymphocyte function
6	1148	19.2	1179	2 115213	integrin alpha-E C
7	1030.5	17.2	1151	2 A45226	integrin alpha-1 C
8	1030.5	17.2	1180	2 A35854	VLA-2 protein homo
9	1012	16.9	1178	2 S44142	integrin alpha-2 B
10	1007.5	16.8	1170	2 145914	integrin alpha-2 C
11	1007.5	16.8	1181	2 A33998	integrin alpha-4 C
12	654.5	10.9	1038	2 S06046	lymphocyte-Peyer's
13	646.5	10.8	1039	2 A41131	alphaP integrin -
14	638	10.7	1054	2 JC7294	integrin alpha-1 C
15	61	10.2	1041	2 731437	integrin alpha-9 C
16	584.5	9.8	1035	2 158409	VLA-3 alpha subuni
17	579.5	9.7	1053	2 155534	cell surface Glyco
18	576.5	9.6	1051	2 A35761	glycoprotein IIb -
19	555	9.3	1037	2 A60163	fibronectin recept
20	552	9.2	1049	2 A27079	integrin alpha-2b
21	548	9.2	1039	2 A34269	integrin alpha-3 C
22	547.5	9.1	1051	2 A40021	integrin alpha-5 C
23	535.5	8.9	1053	2 S44250	integrin alpha-5 C
24	534	8.9	1034	2 A36108	integrin alpha-v C
25	524.5	8.8	1394	2 A29637	position-specific
26	524.5	8.8	1044	2 T10050	integrin alpha-v C
27	496.5	8.3	1072	2 A38457	integrin alpha-6 C
28	493	8.2	1048	2 A27421	integrin alpha-5 C
29	492	8.2	1146	2 S40311	integrin - fruit E

Query 1 TFGTVLILLSVLASYHGFNLD.....DTATFSGDDFSCTVAPNVPPLS 1161

Query 1 TFGTVLILLSVLASYHGFNLD.....DTATFSGDDFSCTVAPNVPPLS 1161

ALIGNMENTS

RESULT 1	PWHUIC	cell surface Glycoprotein CD11c precursor - human	cell surface Glycoprotein CD11c precursor - human receptor p150,95 alpha chain
C:Species: Homo sapiens (man)	C:Species: Homo sapiens (man)	N:Alternate names: leukocyte adhesion receptor p150,95 alpha chain	N:Alternate names: leukocyte adhesion receptor p150,95 alpha chain
C:Accession: A3584; A35543; S00864	C:Accession: A3584; A35543; S00864	C:Accession: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 22-Jun-1999	C:Accession: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 22-Jun-1999
R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.			
J: Biol. Chem. 265, 2782-2788, 1990	J: Biol. Chem. 265, 12750-12751, 1990	J: Biol. Chem. 265, 12750-12751, 1990	J: Biol. Chem. 265, 12750-12751, 1990
A:Reference number: A35543; MUID:90153906; PMID:2303426			
A:Accession: A3584	A:Accession: A3584	A:Accession: A3584	A:Accession: A3584
A:Molecule type: DNA	A:Molecule type: DNA	A:Molecule type: DNA	A:Molecule type: DNA
A:Residues: 1-1163 <COR>	A:Residues: 1-1163 <COR>	A:Residues: 1-1163 <COR>	A:Residues: 1-1163 <COR>
A:Note: this revision to the sequence from reference A35543 includes the carboxyl end	A:Note: this revision to the sequence from reference A35543 includes the carboxyl end	A:Note: this revision to the sequence from reference A35543 includes the carboxyl end	A:Note: this revision to the sequence from reference A35543 includes the carboxyl end
R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.	R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.	R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.	R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
A:Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.	A:Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.	A:Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.	A:Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.
A:Accession: A35543	A:Accession: A35543	A:Accession: A35543	A:Accession: A35543
A:Residues: 1-894 <CO2>	A:Residues: 1-894 <CO2>	A:Residues: 1-894 <CO2>	A:Residues: 1-894 <CO2>
A:Note: this sequence has been revised in reference A36584	A:Note: this sequence has been revised in reference A36584	A:Note: this sequence has been revised in reference A36584	A:Note: this sequence has been revised in reference A36584
R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.	R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.	R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.	R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
E:MB: J. 6 4023-4028, 1987			
A:Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte	A:Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte	A:Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte	A:Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte
A:Reference number: S00864; PMID:3327687			
A:Accession: S00864	A:Accession: S00864	A:Accession: S00864	A:Accession: S00864
A:Residues: 1-755, 'L', 757-1163 <CO3>			
A:Cross-references: GB:MB1695; EMBL:Y00093; NID:91487829; PID:AA59180.1; PMID:91487830			
A:Title: part of this sequence was confirmed by protein sequencing	A:Title: part of this sequence was confirmed by protein sequencing	A:Title: part of this sequence was confirmed by protein sequencing	A:Title: part of this sequence was confirmed by protein sequencing
C:Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on mye	C:Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on mye	C:Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on mye	C:Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on mye
C:Genes:	C:Genes:	C:Genes:	C:Genes:
A:Cross-references: GDB:119758; OMIM:151510	A:Cross-references: GDB:119758; OMIM:151510	A:Cross-references: GDB:119758; OMIM:151510	A:Cross-references: GDB:119758; OMIM:151510
A:Map position: 16p1.2-16p1.2	A:Map position: 16p1.2-16p1.2	A:Map position: 16p1.2-16p1.2	A:Map position: 16p1.2-16p1.2
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo	C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo	C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo	C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo
C:Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat;	C:Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat;	C:Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat;	C:Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat;
F:1-19/Domain: signal sequence #status Predicted <SIG>			
F:20-1163/Domain: extracellular #status Predicted <EXT>			
F:149-319/Domain: von Willebrand factor type A repeat homology <WMA4>	F:149-319/Domain: von Willebrand factor type A repeat homology <WMA4>	F:149-319/Domain: von Willebrand factor type A repeat homology <WMA4>	F:149-319/Domain: von Willebrand factor type A repeat homology <WMA4>
F:1108-1133/Domain: transmembrane #status Predicted <TM>			
F:1134-1163/Domain: intracellular #status Predicted <INT>			
F:61,89,392,697,735,899,939,1030/Binding site: carbohydrate (Asn) (covalent) #status Predicted <CAR>	F:61,89,392,697,735,899,939,1030/Binding site: carbohydrate (Asn) (covalent) #status Predicted <CAR>	F:61,89,392,697,735,899,939,1030/Binding site: carbohydrate (Asn) (covalent) #status Predicted <CAR>	F:61,89,392,697,735,899,939,1030/Binding site: carbohydrate (Asn) (covalent) #status Predicted <CAR>
Query Match Score 3818; DB 1; Length 1163;	Query Match Score 3818; DB 1; Length 1163;	Query Match Score 3818; DB 1; Length 1163;	Query Match Score 3818; DB 1; Length 1163;
Best Local Similarity 65.5%; Pred. No. 6 6e-567;	Best Local Similarity 65.5%; Pred. No. 6 6e-567;	Best Local Similarity 65.5%; Pred. No. 6 6e-567;	Best Local Similarity 65.5%; Pred. No. 6 6e-567;
Matches 755; Conservative 138; Mismatches 253; Indels 6; Gaps 5;	Matches 755; Conservative 138; Mismatches 253; Indels 6; Gaps 5;	Matches 755; Conservative 138; Mismatches 253; Indels 6; Gaps 5;	Matches 755; Conservative 138; Mismatches 253; Indels 6; Gaps 5;

CC BORN PATHOGENS, PARTICULATE MATTER, AND SENESCENT ERYTHROCYTES FROM THE BLOOD.

CC SUBUNIT: HETERO-DIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-D ASSOCIATES WITH BETA-2.

CC SUBCELLULAR LOCATION: Type I membrane protein.

CC TISSUE SPECIFICITY: EXPRESSED MODERATELY ON MYELOMONOCYTIC CELL LINES AND SUBSETS OF PERIPHERAL BLOOD LEUKOCYTES AND STRONGLY ON TISSUE-SPECIALIZED CELLS, INCLUDING MACROPHAGES, FOAM CELLS WITHIN ATHEROSCLEROTIC PLAQUES, AND ON SPLENIC RED PULP MACROPHAGES.

CC DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.

CC SIMILARITY: Belongs to the integrin alpha chain family.

CC SIMILARITY: Contains 1 VWA domain.

CC SIMILARITY: Contains 7 FG-GAP repeats.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR U37028; AAB38547.1; -.

CC DR EMBL; U40224; AAB60634.1; -.

CC DR EMBL; U40225; AAB60635.1; -.

CC DR EMBL; U40226; AAB60636.1; -.

CC DR EMBL; U40227; AAB60637.1; -.

CC DR EMBL; U40229; AAB60638.1; -.

CC DR EMBL; U40228; AAB60638.1; JOINED.

CC DR EMBL; A187881; AAF62875.1; -.

CC DR HSSP; P11215; 1ABX.

CC DR Genew; HGNC; 6146; ITGAD.

CC DR MIM; 602452; -.

CC DR GO; GO:0008405; C:integrin complex; TAS.

CC DR GO; GO:004495; F:cell adhesion receptor activity; TAS.

CC DR GO; GO:0015337; P:cell-cell adhesion; NAS.

CC DR GO; GO:0007160; P:cell-matrix adhesion; NAS.

CC DR PRINTS; PRO0185; INTEGRINA.

CC DR InterPro; IPR000413; Integrin_alpha.

CC DR InterPro; IPR002035; VWF_A.

CC DR Pfam; PF01839; FG-GAP; 3.

CC DR Pfam; PF00357; integrin_A; 1.

CC DR Pfam; PF00092; vwa; 1.

CC DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.

CC DR PROSITE; PS00234; VWF_A; 1.

CC KW Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane; Signal; Repeat; Calcium; Magnesium.

CC FT SIGNAL; 1 17 POTENTIAL.

CC FT CHAIN; 18 1162 INTEGRIN ALPHA-D.

CC FT DOMAIN; 18 1100 EXTRACELLULAR (POTENTIAL).

CC FT TRANSMEM; 1101 1124 POTENTIAL.

CC FT DOMAIN; 1125 1162 CYTOPLASMIC (POTENTIAL).

CC FT REPEAT; 32 85 FG-GAP 1.

CC FT REPEAT; ? ? FG-GAP 2.

CC FT DOMAIN; 150 332 VMPA.

CC FT REPEAT; 350 400 FG-GAP 3.

CC FT REPEAT; 401 452 FG-GAP 4.

CC FT REPEAT; 454 516 FG-GAP 5.

CC FT REPEAT; 518 576 FG-GAP 6.

CC FT REPEAT; 581 633 FG-GAP 7.

CC FT CA_BIND; 465 473 POTENTIAL.

CC FT CA_BIND; 530 538 POTENTIAL.

CC FT REPEAT; 593 601 POTENTIAL.

CC FT SITE; 1127 1131 GFFRR MOTIF.

CC FT DISULFID; 67 74 BY SIMILARITY.

CC FT DISULFID; 106 124 BY SIMILARITY.

CC FT DISULFID; 655 710 BY SIMILARITY.

FT DISULFID 769 775 BY SIMILARITY.

FT DISULFID 846 861 BY SIMILARITY.

FT DISULFID 994 1018 BY SIMILARITY.

FT DISULFID 1023 1028 BY SIMILARITY.

FT CARBOHYD 559 559 (POTENTIAL).

FT CARBOHYD 87 87 (POTENTIAL).

FT CARBOHYD 99 99 (POTENTIAL).

FT CARBOHYD 391 391 (POTENTIAL).

FT CARBOHYD 691 691 (POTENTIAL).

FT CARBOHYD 733 733 (POTENTIAL).

FT CARBOHYD 873 873 (POTENTIAL).

FT CARBOHYD 957 957 (POTENTIAL).

FT CARBOHYD 1046 1046 (POTENTIAL).

FT CONFLICT 500 500 MISSING (IN REF. 2).

FT CONFLICT 515 518 GHPW -> ATP (IN REF. 2).

FT CONFLICT 825 825 L -> V (IN REF. 2).

FT CONFLICT 984 984 V -> A (IN REF. 2).

FT SEQUENCE 1162 AA; 126885 MW; F296ALA35455D7D CRC64;

Query Match 100.0% Score 5987; DB 1; Length 1162;

Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0; Mismatches 0; Matches 1161; Conservative 0;

Qy 1 TPGVVLISVLVSLAYHGPMLDVEEPTFQEDAGGGQEVVQFGGSVWVGGSRVAGPLEVAANT 60

Db 2 TPGVVLISVLVSLAYHGPMLDVEEPTFQEDAGGGQEVVQFGGSVWVGGSRVAGPLEVAANT 61

Qy 61 GRLYDCAAATGMQCPPIPHIRPEAVNMSGLTIAAESTNGSRLAACPTLHRVCGENYSK 120

Db 62 GRLYDCAAATGMQCPPIPHIRPEAVNMSGLTIAAESTNGSRLAACPTLHRVCGENYSK 121

Qy 121 GSCILLGSRWEIITQTPATPCPHQMDIVPLIDSGSITONDENCMKGFYQAVNGQFE 180

Db 122 GSCILLGSRWEIITQTPATPCPHQMDIVPLIDSGSITONDENCMKGFYQAVNGQFE 181

Qy 181 GDTDLFALM0QSNLILKHTFQFRTSQQSLDPIVQKLTFTATGILITVTVQTLFHH 240

Db 182 GDTDLFALM0QSNLILKHTFQFRTSQQSLDPIVQKLTFTATGILITVTVQTLFHH 241

Qy 241 KNGARKSAKAKLIVITDQKQDPLESDVPOAEEKAGIRVAVGCHAFQOPTAROLEN 300

Db 242 KNGARKSAKAKLIVITDQKQDPLESDVPOAEEKAGIRVAVGCHAFQOPTAROLEN 301

Qy 301 TISSAPPQDHDVFKDNFAALGSIQKLODEKIVAYEGTQGRASSFSQHMSQEGFSTATLM 360

Db 302 TISSAPPQDHDVFKDNFAALGSIQKLODEKIVAYEGTQGRASSFSQHMSQEGFSTATLM 361

Qy 361 DGLFLGAYGSFSWGGAAFLPPNMSPTINMSQENMDTSVLYSTELALMKGVQNLVL 420

Db 362 DGLFLGAYGSFSWGGAAFLPPNMSPTINMSQENMDTSVLYSTELALMKGVQNLVL 421

Qy 421 GAPPYQHTGKAVIIFTQSRWRAKAEVGTGQTSYFASLCSVDGSDTPLILIGPH 480

Db 422 GAPPYQHTGKAVIIFTQSRWRAKAEVGTGQTSYFASLCSVDGSDTSDLILIGPH 481

Qy 481 YYEQTRGGQSVCPLRGQVQOCDAYLVRGEOGHPMGRGFAALTVLGVDNEEDKLTDVAI 540

Db 482 YYEQTRGGQSVCPLRGQVQCDAYLVRGEOGHPMGRGFAALTVLGVDNEEDKLTDVAI 541

Qy 541 GAPPGEQENRGAVYLFGHASESGISPSHQSRIASSQSLSPRLQYFGOALSQDGTODGMD 600

Db 542 GAPPGEQENRGAVYLFGHASESGISPSHQSRIASSQSLSPRLQYFGOALSQDGTODGMD 601

Qy 601 LAVGARGQVLLRSLPVLKVGAMRFSPVEVAKAVYREEKWEEKPSALEGDATCLTICKS 660

Db 602 LAVGARGQVLLRSLPVLKVGAMRFSPVEVAKAVYREEKWEEKPSALEGDATCLTICKS 661

Qy 661 SLDQGDGQSVRFDLADPGRITSRAIFNETKNPTRKTKLGLGIHETLKLLPPCV 720

Db 662 SLDQGDGQSVRFDLADPGRITSRAIFNETKNPTRKTKLGLGIHETLKLLPPCV 721

Qy 721 EDVYSPILHNLNSLVEREPSPONLRYPLVAVSQDLETTASLPEKONGQDGLCEGDGV 780

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2004, 09:36:23 ; Search time 56 Seconds (without alignments)

Scoring table: BLOSUM62

Title: US-09-891-943-2

Perfect score: 5987

Sequence: 1 TGTGTVLLSVLASTHGFNLD.....DTATFSSGDDFSCVAPNVPIS 1161

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqB, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 23:**

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

SPTREMBL 23:**

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4415.5	73.8	1161	1 Q9OYE7	Q9OYE7 rattus norv
2	3824.4	63.9	1169	4 Q8IVAE	Q8IVAE rattus norv
3	3581.5	59.8	1169	11 Q9QXH4	Q9QXH4 rattus norv
4	3314.4	55.4	1151	11 Q9J130	Q9J130 rattus norv
5	2829.9	47.3	920	6 Q28984	Q28984 sus scrofa
6	2755.6	46.0	1036	11 Q8CA73	Q8CA73 mus musculu
7	1451.5	24.2	1161	11 Q9WTV4	Q9WTV4 mus musculu
8	1447.0	24.2	1160	11 Q9R200	Q9R200 mus musculu
9	1318.8	22.0	1086	4 Q96HBI	Q96HBI ratti
10	1297.5	21.7	1196	13 Q98TF1	Q98TF1 cyprinus ca
11	1263.3	21.1	1187	13 Q98TF0	Q98TF0 cyprinus ca
12	1220.5	20.4	927	6 Q8HZV0	Q8HZV0 bos taurus
13	1164.5	19.5	1167	11 Q8340	Q8340 rattus norv
14	1138.5	19.0	1167	11 Q88341	Q88341 rattus norv
15	1096.5	18.3	1188	11 Q7TC03	Q7TC03 mus musculu
16	1041.1	17.4	1171	13 Q42094	Q42094 gallus gal

Q8TESS homo sapien
Q8bs01 mus musculu
Q9wif8 mus sp. itg
Q8mkf4 felis silve
Q9pqb8 halocyynthia
Q9WY8 homo sapien
Q8ce84 mus musculu
Q81899 mus musculu
Q62781 xenopus lae
Q96s81 strongyloce
Q9g987 pseudoplusi
Q82270 ratti

Q9g3001 ratetus norv
Q9g303 bos taurus
Q9lyd5 mus musculu
Q98ct7 gallus gall
Q9b90 lytechinus
Q73378 lytechinus
Q8c270 mus musculu
Q7yyp8 equus cabal
Q9tun4 oryctolagus
Q91779 xenopus lae
Q8t95 mus musculu
Q86g88 pseudoplusi
Q8b182 homo sapien
Q70304 mus musculu
Q9g48 bos taurus
Q42598 xenopus lae
Q8551 drosophila
Q9mzd6 bos taurus

ALIGNMENTS

RESULT 1

Q9OYE7 PRELIMINARY; PRT; 1161 AA.

ID Q9OYE7 PRELIMINARY; PRT; 1161 AA.

AC Q9OYE7; DT 01-MAY-2000 (TREMBLref. 13, Created)

DR 01-MAY-2000 (TREMBLref. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLref. 13, Last annotation update)

DR 01-JUN-2003 (TREMBLref. 24, Last annotation update)

DE Alpha D integrin.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Murinae; Muridae; Rattus. NCBI_TaxID:10116; [1]

ON [1]

RP SEQUENCE FROM N.A.

RC STRAINS-Sprague-Dawley;

RA O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietrich G., Gallatin W.M.;

RT "Cloning of rat alpha D, a novel beta 2 integrin.";

RL Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF021334; AFAF21241.1; -

DR HSSP; P11215; IEBHQ; C:integrin complex; IEA.

DR GO; GO_0008305; C:integrin complex; IEA.

DR GO; GO_0004895; P:cell adhesion receptor activity; IEA.

DR GO; GO_0007160; P:cell-matrix adhesion; IEA.

DR InterPro; IPR00413; Integrin_alpha.

DR InterPro; IPR003035; WWP_1.

DR Pfam; PF01839; EG-GAT; 3.

DR Pfam; PF00357; Integrin_A; 1.

DR Pfam; PF00092; WWA; 1.

DR PRINTS; PR01185; INTEGRINA.

DR PRINTS; PR00453; WVFADOMAN.

DR SMART; SM00191; Int_alpha; 4.

DR SMART; SM00277; VWA; 1.

DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.

DR PROSITE; PS50234; VWFPA; 1.

KW Integrin.

SQ SEQUENCE 1161 AA; 126600 MW; 2258491A984A705E CRC64; 8Q

Qy	3	GTVLSS -VLA3YHGFNDVEEPTIDFDBAGFGOSVYQFGCSRLVYGAPELVAANQT	60	Db	1021 DCLHFRCDIFPSLDIODEDFDIFRGNLNSGWSVSLQEVYLISBAAETFDTSVYSQLFGQ	1080
Best Local Similarity	73.8%	Score 4415.5;	DB 11;	Length 1161;		
Matches	853;	Pred. No. 0;				
Matches	853;	Conservative 111;	Indels	5;	Gaps	4;
Qy	4	GVVILLCGVNLVASHGSNLIDVEEPIVPRBDASFQTVQFGCSRLVYGAPELVAANQT	63	Qy	1081 EAFRAQMEMVLEDEDVNAIPIMGSYGAIIIAITATLYKLGFPRHYKEMLEDKP	1140
Db	61	GLYDCAATGMCOPIPHIRPAVAVNSLGLTIAASTGSRLLACGPTLHRCVGENSYSK	120	Db	1081 EAFRAQVTTLEXYVYBPIFYAVGSYGGIILLLATTVVYKLGFPRYKEMLEDKA	1140
Db	64	GLYDCAPATGMCOPIVLRSPLEAVMSLGLSLVATNAQIACGPTAQACVROMYAK	123			
Qy	121	GSCUHLGERWEIITQTPDAPTECPHQENDIVFLDGGISIDONDFTNOMKGKQAMGQFE	180			
Db	124	GSCUHLGGSLQFOAVPAMPECPQENDIAFLDGGISINQDFDAMKDVKALMGEA	183	Q8IVY6	PRELIMINARY;	PRT;
Qy	181	GTDPLFLAMQYSNLKTHFTFTQFRTSPSQSISLVDPIVOLQKLTETATGILTVTUVOLFHH	240	ID	Q8IVY6;	
Db	184	STISLFLSMLQYSNLKTHFTFTKLNIDPQSLVDPVQLOLQDITYATGILTVMEBLFS	243	AC	Q8IVY6;	
Qy	241	KGNGARKSACKLILVITDQKXKDPPLYESDVIPOAEGKIGIIRYAIYCHAFQGPTAROELN	300	DT	01-MAR-2003 (TREMBLrel. 23; Created)	
Db	244	KGNGARKSACKLILVITDQKXKDPPLYESDVIPOAEGKIGIIRYAIYCHAFQGPTAROELN	303	DT	01-MAR-2003 (TREMBLrel. 23; Last sequence update)	
Qy	301	TISSAPPDQHVFRTDNFALGSIQKQLOEKIYAVEGTOSRASSPQEMSGFGSTALM	360	DR	01-OCT-2003 (TREMBLrel. 25; Last annotation update)	
Db	304	TIGSAPPDQHVFRTKYGNAFLRSQRLQEKIYAEIGTOSRASSPQEMSGFGSSALTS	363	DR	Integrin, alpha X (Antigen CD11C (p150), alpha polypeptide).	
Qy	361	DGIFLGLAVESFSWGGAFAYPPNMSPTTINMSDENTMDRSTYGYSTELAWLKGYONLVL	420	DR	Homo Sapiens (Human).	
Db	364	DGPVIGAVSFSSGGATLYPPNTRPTTINMSDENTMDRSTYGYSTAVATWKGHSLIL	423	DR	Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Qy	421	GAPYQHQTCKAVIIFTQVSQRWIKAAEVTTGTOIGSYFGASLCSYDVTDSGSTDLLIGAPH	480	DR	Mammalia; Eutheria; Primates; Catarrhini; Homiridae; Homo.	
Db	424	GAPHQHQTCKAVIIFTQVSQRWIKAAEVTTGTOIGSYFGASLCSYDVTDBDGSSTDVLIGAPH	483	DR	NCBI_TaxID: 9606;	
Qy	481	YYEOTRGCGSYVCPLPREGVRVOCDAVLRGCHPGRGAALTVLGVDNEKDJKLIDVAI	540	RN	RN	
Db	484	YYEOTRGCGSYVCPLPREGVRVOCDAVLRGCHPGRGAALTVLGVDNEKDJKLIDVAI	542	RP	SEQUENCE FROM N.A.	
Qy	541	GAPGEQENRGAYVLLFHGASCSGSPSHSORIASSQSLSPRLYFQGALSGQGDLTQDGIMD	600	RC	TISSUE=Blood;	
Db	543	GAPEEEERSGAVTIFHGASRLLEMPSPQRTVSQSLRQFQGQSLDQPLTQGLVD	602	RA	Strasbourg, R.	
Qy	601	LAVARGQVLLSLPLVKYGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVCLTIQK	660	RL	Submitted (SSB-2002) to the EMBL/GenBank/DBJ databases.	
Db	603	LAVGAQHVLILSLPLVKVELSLRFAELMEVAKAVYRCWERTPTVLEAGATVCLTVHKG	662	DR	EMBL: BC038237; AAH38237.1;	
Qy	661	SLDLDGDIOSVREPLADPGRILTSRALFENYKPLTRRTRGHLGHCTKLLPDCV	720	DR	GO; GO:0008305; C: integrin complex; IFA.	
Db	663	SPDILGNYGQSYRDYLDLPGRLTSRAFDETKNCLTGRKTGL3HCTKLLPDCV	722	DR	GO; GO:004895; F: cell adhesion receptor activity; IFA.	
Qy	721	EDVSPITLHLNFSLVREPIPSQNLSPVYKPLTRRTRGHLGHCTKLLPDCV	780	DR	InterPro: IPR00413; Integrin_alpha.	
Db	723	EDVSPITLHLNFSLVRS-ASPRNLHVTAVGQDHTASLPEKNCQELCSDGLI	781	DR	InterPro: IPR00415; VWP_A.	
Qy	781	TLSFSGLQTLTVGSESLNLNVITVWNAGBDSYGTVVSLYPPAGLSHRVSQAKOPHOA	840	DR	Pfam: PF01839; FG-GAP; 3.	
Db	782	SFNSFGLQVLUVVGSPSPLTVTVWNEDSISGTLVKKYPPGLSSTERVGTQ-QHQP	840	DR	Pfam: PF00357; integrin_A; 1.	
Qy	841	LRLACETVTEDEGLRSRCSVYHPIFHEGSNQTFIVTFDVSYKATLGDRMMRASASSE	900	DR	Pfam: PF00092; vwa_1.	
Db	841	LRACEAEPAQELPRLSSCSINHPIFEGAKITFMTDVSYKAFGDRLLRACASSE	900	DR	PRINTS: PR01185; INTEGRINA.	
Qy	901	NNKASSKKATTFQELPLPVYKAYVIMISROBESITKXENFATSDEKMKMKAEEHRYVNLSQR	960	DR	SMART: SM00327; vwa_1.	
Db	901	NNKEDDTNKAQELPLPVYKAYVIMISROBESITKXENFATSDEKMKMKAEEHRYVNLSPL	960	DR	PROSITE: PS007160; P16043; Integrin_alpha.	
Qy	961	DLAISINFNTWVPLVINGVAVWDYMEAPQLPCTSERKPPQHSDPDLTQISSPMLDCSIA	1020	DR	SEQUENCE FROM N.A.	
Db	961	KLAIRVNPNVWVPLVINGVAVWDYTLSSPAGQVSCYSONKPKPQNDTQIQRSVLDCCSIA	1020	DR	Score 3024; DB 4; Length 1169;	
Qy	1021	DCLQFRCDVPSFSVQSEELDFTLKGNLISFGWVRETLQKKVYVVAETFDTSVYSQLPGQ	1080	DR	Best Local Similarity 65.8%; Pred. No. 4.6e-285; Matches 758; Conservative 135; Mismatches 253; Indels 6; Gaps 5;	
			Qy	1 TFGTLLSLVSLASTHGFNIDVEETTIFEDAGFGQSTVQFGCSRLVYGAPELVVANQ	60	
			Db	4 TRAALIIFPLATLSLGFNIDTELTAFRYDTSAGFGDSVSYQANSWVVGAPQKITAANQT	63	
			Qy	61 GLYDCAATGMCOPIPHIRPAVAVNSLGLTAASTGSRLLACGPTLHRCVGENYSK	120	
			Db	64 GGLYQGYSGACBPGIGVPPHEGRNMLT	123	
			Qy	121 GSCUHLGERWEIITQTPDAPTECPHQENDIVFLDGGISIDONDENQMKGFIQAVMGCFE	180	
			Db	124 GLCFLPGLPTQLTQRLPVSQECRQEDPQDIFVLDGSSSISSRNATMNFYRAVISQ	182	
			Qy	181 GTDILFALQYNSNLKINHFTQRTTSQQLDPIVOLKGJPTTARGILTVTQLRH	240	
			Db	183 RPSQTSFLQFSNKEQHTTFFEEFRSSNPLSLASVHQGFTYATARIQVYHRLPFA	242	
			Qy	241 RNGARKSARKLILVITDQKXKDPPLYESDVIPOAEGKIGIIRYALGVGAFOQGPATOLN	300	
			Db	243 SYGARTRAKKILVITDQKXKDPPLYESDVIPOAEGKIGIIRYALGVGAFOQGPATOLN	302	
			Qy	301 TISSAPPDQHVFRTDNFALGSIQKQLOEKIYAVEGTOSRASSFQHQSQEFSTALTM	360	
			Db	303 DIASKPQHIFKVTEDFALKDIONQLKEKIPATEGETTSSSSPELMAEQGSVAFTP	362	

GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2004, 09:32:28 ; Search time: 65 Seconds

(without alignments)
5046.733 Million cell updates/sec

Title: US-09-891-943-2

Perfect score: 5987

Sequence: 1 TGTIVLLSVLASYHGFNLDDDDFSCVAPNVPPLS 1161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:
1: geneseqP1990s:
2: geneseqP1990s:
3: geneseqP2000s:
4: geneseqP2001s:
5: geneseqP2000s:
6: geneseqP2003as:
7: geneseqP2003bs:
8: geneseqP2004s:
AAR78166

Post-processing: Minimum Match 0%
Listing first 45 summaries

1: 5987 100.0 1161 2 AAR78166
2: 5987 100.0 1161 2 AAW23049
3: 5987 100.0 1161 2 AAW57491
4: 5987 100.0 1161 2 AAW72825
5: 5987 100.0 1161 3 AAB07359
6: 5987 100.0 1161 5 ABB61468
7: 5981 99.9 1161 2 AAW65089
8: 5981 99.9 1161 2 AAW73342
9: 5971.5 99.7 1161 2 AAW23064
10: 5971.5 99.7 1161 2 AAW55106
11: 5971.5 99.7 1161 2 AAW72837
12: 5971.5 99.7 1161 2 AAW73343
13: 5971.5 99.7 1161 3 AAB07376
14: 5971.5 99.7 1161 5 ABG61485
15: 4403.5 73.6 1161 2 AAW23162
16: 4403.5 73.6 1161 2 AAW60004
17: 4403.5 73.6 1161 2 AAW72824
18: 4403.5 73.6 1161 3 AAB07374
19: 4403.5 73.6 1161 5 ABG61483
20: 4397.5 73.5 1161 2 AAW65104
21: 4395.5 73.5 1161 2 AAW73345
22: 4395.5 73.4 1161 2 AAR71619
23: 4365.5 72.9 1151 2 AAR78179
24: 4364.5 72.9 1151 2 AAW22059
25: 4364.5 72.9 1151 2 AAW60001

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	5987	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	100.0	1161	2	AAR78166	Aar78166 Human bet
2	5987	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	100.0	1161	2	AAW23049	Aaw23049 Human bet
3	5987	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	100.0	1161	2	AAW57491	Aaw57491 Human bet
4	5987	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	100.0	1161	2	AAW72825	Aaw72825 Human alp
5	5987	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	100.0	1161	3	AAB07359	Aab07359 Human alp
6	5987	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	100.0	1161	5	ABB61468	Abb61468 Human Bet
7	5981	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	99.9	1161	2	AAW65089	Aaw65089 Human Bet
8	5981	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	99.9	1161	2	AAW73342	Aaw73342 Human alp
9	5971.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	99.7	1161	2	AAW23064	Aaw23064 Human bet
10	5971.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	99.7	1161	2	AAW55106	Aaw55106 Human Bet
11	5971.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	99.7	1161	2	AAW72837	Aaw72837 Human alp
12	5971.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	99.7	1161	2	AAW73343	Aaw73343 Human alp
13	5971.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	99.7	1161	3	AAB07376	Aab07376 Human alp
14	5971.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	99.7	1161	5	ABG61485	Abg61485 Human Bet
15	4403.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	73.6	1161	2	AAW23162	Aaw23162 Rat beta
16	4403.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	73.6	1161	2	AAW60004	Aaw60004 Rat alpha
17	4403.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	73.6	1161	2	AAW72824	Aaw72824 Rat alpha
18	4403.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	73.6	1161	3	AAB07374	Aab07374 Rat alpha
19	4403.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	73.6	1161	5	ABG61483	Abg61483 Rat Beta2
20	4397.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	73.5	1161	2	AAW65104	Aaw65104 Rat beta
21	4397.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	73.5	1161	2	AAW73345	Aaw73345 Rat alpha
22	4395.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	73.4	1161	2	Aar78169	Aar78169 Rat alpha
23	4365.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	72.9	1151	2	AAW78179	Aaw78179 Rat alpha
24	4364.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	72.9	1151	2	AAW22059	Aaw22059 Rat beta
25	4364.5	A_Geneseq_29Jan04: 1: geneseqP1990s: 2: geneseqP1990s: 3: geneseqP2000s: 4: geneseqP2001s: 5: geneseqP2000s: 6: geneseqP2003as: 7: geneseqP2003bs: 8: geneseqP2004s: AAR78166	72.9	1151	2	AAW60001	Aaw60001 Rat alpha

ALIGNMENTS

RESULT 1							
ID	XX	AC	XX	XX	DE	DE	XX
AAR78166	XX	AAR78166;	XX	XX	DT	28-DEC-1995	(first entry)
					DE	Human beta-2 integrin alpha-d.	
					XX	Beta-2 integrin alpha-h subunit; antiinflammatory; arteriosclerosis; inflammatory bowel disease; asthma.	
					XX	Homo sapiens.	
					XX	Key	Location/Qualifiers
						17-1108	/note= "extracellular domain"
						150-.352	
							/note= "this region is homologous to the insert common to CH11a,b,c and may be a site for interaction with ICM family proteins"
					FT	Binding-site	465-.474
							/note= "putative cation binding site"
					FT	Binding-site	518-.527
							/note= "putative cation binding site"
					FT	Binding-site	592-.600
							/note= "putative cation binding site"
					FT	Region	1109-.1128
							/note= "transmembrane region"
					FT	Domain	1129-.1161
							/note= "cytoplasmic domain"
					XX	W09517412-A1.	
					PD	29-JUN-1995.	
					XX	21-DEC-1994;	
					XX	23-DEC-1993;	93US-00173497.
					PR	05-AUG-1994;	94US-00173497.
					XX	05-AUG-1994;	94WO-US014832.
					XX		(ICOS-) ICOS CORP.
					PI		Gallatin WM, Van Der Vieren M;
					XX		
					DR	WPI: 1995-240603/31.	
					DR	N-PSDB; ARQ91712.	

Alpha sub-unit polypeptide of human beta 2 integrin - used to identify potential antiinflammatory agents, for the treatment of graft arteriosclerosis, inflammatory bowel disease, asthma, etc. Claim 7: Page 82-87; 172PP; English.

A probe based on a partial cDNA clone (given in AAQ91727) of canine alpha-TM1 was used to screen a human spleen cDNA library to identify clone 19A2 encoding the beta-1 integrin alpha subunit, alpha-d. The cDNA is composed of 1116 nucleotides and has a calculated molecular weight of 39.5 kDa.

RESULT 2
US-09-891-943-2
Application US/09891943
Publication No. US20030077278A1
GENERAL INFORMATION
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20030077278A1el Human 2
FILE REFERENCE: 21866725004
CURRENT APPLICATION NUMBER: US/09/891, 943
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 09/193, 043
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/286, 889
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 08/362, 652
PRIOR FILING DATE: 1994-12-11
PRIOR APPLICATION NUMBER: 08/943, 363
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 2
LENGTH: 1161
TYPE: PRT
ORGANISM: Homo sapiens
US-09-891-943-2

Query Match 100.0%; Score 5987; DB 10; Length 1161;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TFGTYLILSVLASYHGFMLVDEEPTIPOEDAGGFGSVYQFGSRLVYVGAPLEVVAAQT 60
DB 1 TFGTYLILSVLASYHGFMLVDEEPTIPOEDAGGFGSVYQFGSRLVYVGAPLEVVAAQT 60
QY 61 GRUYDCAATGMQPIPHIRPAVAVNSLGTIAASTNSGRSLIACGPTLHRVGENYSK 120
DB 61 GRUYDCAATGMQPIPHIRPAVAVNSLGTIAASTNSGRSLIACGPTLHRVGENYSK 120
QY 121 GSCLLIGRMELIQTIVATATPCHQMDIVFLIDGSSIDIDNDNOMKGFYQAVNGQPE 180
DB 121 GSCLLIGRMELIQTIVATATPCHQMDIVFLIDGSSIDIDNDNOMKGFYQAVNGQPE 180
QY 181 GTDILFAMQYSNLLKHFPTFQRTSDQSLSLYDPIVQLKLTFTATGILTVTQLFHH 240
DB 181 GTDILFAMQYSNLLKHFPTFQRTSDQSLSLYDPIVQLKLTFTATGILTVTQLFHH 240
QY 721 EDVSPILLHNLNSLYREPIPSQNLRLPVLAVGSDLFTASLPFEKNCQGDGLCERGLGV 780
DB 721 EDVSPILLHNLNSLYREPIPSQNLRLPVLAVGSDLFTASLPFEKNCQGDGLCERGLGV 780
QY 781 TLFSGIQTLYTGSSELEINVITVWANGEDSYGTIVSLLYDAGLSHRSVSGAQKOPHOQA 840
DB 781 TLFSGIQTLYTGSSELEINVITVWANGEDSYGTIVSLLYDAGLSHRSVSGAQKOPHOQA 840
QY 901 NNKASSKATFOLELPKYAVTMISQEESTKYNPATSEKOKMKEAHRYVNLNSQR 960
DB 901 NNKASSKATFOLELPKYAVTMISQEESTKYNPATSEKOKMKEAHRYVNLNSQR 960
QY 961 LRLACETPTDEGLRSRCSYHPIHEGSNGTFIVTEDSYKATLGDRMLMRASASSE 900
DB 961 LRLACETPTDEGLRSRCSYHPIHEGSNGTFIVTEDSYKATLGDRMLMRASASSE 900
QY 961 DLAISINFNPVILLGAVWDYMEASQSLPCVSRKPPQHSDFLTQISSPMDCSIA 1020
DB 961 DLAISINFNPVILLGAVWDYMEASQSLPCVSRKPPQHSDFLTQISSPMDCSIA 1020
QY 1021 DCLQFRCDVPFSFSYQEBELDFTLKGNLNSLFGWRETQKVLVYVAETEDTSVYSLPGQ 1080
DB 1021 DCLQFRCDVPFSFSYQEBELDFTLKGNLNSLFGWRETQKVLVYVAETEDTSVYSLPGQ 1080
QY 1081 EAFAKQAEQMVLBDEDEVNAIPTIMGSVYGAJLLALITATYKLGFFKRHKEMLEDKP 1140
DB 1081 EAFAKQAEQMVLBDEDEVNAIPTIMGSVYGAJLLALITATYKLGFFKRHKEMLEDKP 1140
QY 1141 EDTATFSGDDFSCVAPNPLS 1161
DB 1141 EDTATFSGDDFSCVAPNPLS 1161

GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2004, 09:37:59 : Search time 23 Seconds
(without alignments)

2605.989 Million cell updates/sec

Title: US-09-891-943-2

Perfect score: 5987

Sequence: 1 TFGTIVLLSVLASTHGFNLD.....DTATFSSDDFSCVAPNVPPLS 1161

Scoring table: BLOSUM62

Gapopen 10.0 , Gapext 0.5

Searched:

389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6_ptodata/2/iaa/5A_COMBO.pep:*

2: /cgn2_6_ptodata/2/iaa/5B_COMBO.pep:*

3: /cgn2_6_ptodata/2/iaa/6A_COMBO.pep:*

4: /cgn2_6_ptodata/2/iaa/6B_COMBO.pep:*

5: /cgn2_6_ptodata/2/iaa/PCITS_COMBO.pep:*

6: /cgn2_6_ptodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Result No.	Score	Query	Match	Length	DB	ID	Description		
							Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli
1	5987	100.0	1161	3	US-09-193-043-2				
2	5987	100.0	1161	4	US-09-688-307A-2				
3	5987	100.0	1161	4	US-09-350-259-2				
4	5981	99.9	1161	1	US-08-173-4-97-2				
5	5981	99.9	1161	1	US-08-288-99-2				
6	5981	99.9	1161	1	US-08-485-618-2				
7	5981	99.9	1161	1	US-08-362-552-2				
8	5981	99.9	1161	2	US-08-605-672-2				
9	5981	99.9	1161	2	US-08-482-293A-2				
10	5981	99.9	1161	2	US-08-943-363-2				
11	5971.5	99.7	1161	1	US-08-485-618-99				
12	5971.5	99.7	1161	1	US-08-605-672-19				
13	5971.5	99.7	1161	2	US-08-482-293A-99				
14	5971.5	99.7	1161	2	US-08-943-363-19				
15	5971.5	99.7	1161	3	US-09-350-259-55				
16	5971.5	99.7	1161	4	US-09-688-307A-99				
17	5971.5	99.7	1161	4	US-09-350-259-99				
18	4403.5	73.6	1161	3	US-08-193-043-55				
19	4403.5	73.6	1161	4	US-09-688-307A-55				
20	4403.5	73.6	1161	4	US-09-350-259-55				
21	4397.5	73.5	1161	1	US-08-485-618-55				
22	4397.5	73.5	1161	1	US-08-362-652-55				
23	4397.5	73.5	1161	2	US-08-605-672-55				
24	4397.5	73.5	1161	2	US-08-482-293A-55				
25	4397.5	73.5	1161	2	US-08-943-363-55				
26	4364.5	72.9	1151	1	US-08-286-889-37				
27	4364.5	72.9	1151	1	US-08-485-618-37				

ALIGNMENTS

RESULT 1
US-09-193-043-2
/ Sequence 2, Application US/09193043
/ Patent No. 6251315
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 62513961 Human 2
/ FILE REFERENCE: 27B66/35004
/ CURRENT APPLICATION NUMBER: US/09/193, 043
/ CURRENT FILING DATE: 18-11-16
/ EARLIER APPLICATION NUMBER: 08/173, 497
/ EARLIER FILING DATE: 1993-12-23
/ EARLIER APPLICATION NUMBER: 08/286, 889
/ EARLIER FILING DATE: 1994-08-05
/ EARLIER APPLICATION NUMBER: 08/362, 652
/ EARLIER FILING DATE: 1994-12-21
/ EARLIER APPLICATION NUMBER: 08/943, 363
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 2
/ LENGTH: 1161
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-193-043-2
Query Match 100.0%; Score 5987; DB 3; Length 1161;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1161; Conservative 0; Sensitive 0;
Qy 1 TFGTIVLLSVLASTHGFNLD.....DTATFSSDDFSCVAPNVPPLS 1161
Db 1 TFGTIVLLSVLASTHGFNLD.....DTATFSSDDFSCVAPNVPPLS 1161
Qy 61 GRLYDAATTEMCPQLPHIREPAANMSLGLTLAATNGSRLLAGPTLHRVCGENYSK 120
Db 61 GRLYDAATTCNCQPLPHIREPAANMSLGLTLAATNGSRLLAGPTLHRVCGENYSK 120
Qy 181 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 181 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 182 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 182 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 183 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 183 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 184 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 184 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 185 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 185 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 186 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 186 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 187 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 187 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 188 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 188 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 189 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 189 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 190 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 190 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 191 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 191 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 192 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 192 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 193 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 193 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 194 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 194 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 195 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 195 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 196 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 196 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 197 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 197 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 198 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 198 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 199 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 199 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 200 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 200 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 201 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 201 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 202 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 202 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 203 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 203 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 204 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 204 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 205 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 205 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 206 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 206 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 207 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 207 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 208 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 208 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 209 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 209 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 210 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 210 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 211 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 211 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 212 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 212 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 213 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 213 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 214 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 214 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 215 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 215 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 216 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 216 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 217 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 217 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 218 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 218 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 219 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 219 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 220 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 220 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 221 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 221 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 222 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 222 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 223 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 223 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 224 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 224 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 225 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 225 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 226 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 226 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 227 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 227 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 228 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 228 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 229 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 229 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 230 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 230 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 231 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 231 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 232 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 232 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 233 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 233 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 234 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 234 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 235 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 235 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 236 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 236 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 237 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 237 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 238 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 238 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 239 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 239 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 240 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 240 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 241 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 241 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 242 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 242 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 243 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 243 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 244 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 244 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 245 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 245 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 246 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 246 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 247 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 247 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 248 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 248 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 249 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 249 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 250 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 250 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 251 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 251 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 252 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 252 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 253 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 253 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 254 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 254 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 255 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 255 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 256 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 256 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Qy 257 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Db 257 GDTDLPAIMQYSNLKIHFTQFTTSPSQSLYDPIVOLKGLTATGTLTYVQLFH 240
Qy 258 GSCLLIGSRWIIICITYPDATECPHQEMDYLIDGGSSTDQDNQMGFVQAVMGQFE 180
Db 258 GSCLLIGSRWIIICITYPDATECPHQEMD

301 TISSAPPQDHVFKVTDNEAALGSIQKQLOEKIYAVEGTSRASSSFQHEMSQEGFSTALTM 360
 301 TISSAPPQDHVFKVTDNEAALGSIQKQLOEKIYAVEGTSRASSSFQHEMSQEGFSTALTM 360
 Db DGLPLGAVGSFSNNGGATLYPPNSPPTINMSQENTMDRDSLGYSTELAWKGVNLVL 420
 Qy 361 DGLPLGAVGSFSNNGGATLYPPNSPPTINMSQENTMDRDSLGYSTELAWKGVNLVL 420
 Db DGLPLGAVGSFSNNGGATLYPPNSPPTINMSQENTMDRDSLGYSTELAWKGVNLVL 420
 Qy 421 GAPYQHTGKAVIPTQSVQRWCKAETGTQGTSYFGASLCSVTDSDGSTDLLIGAPH 480
 Db 421 GAPYQHTGKAVIPTQSVQRWCKAETGTQGTSYFGASLCSVTDSDGSTDLLIGAPH 480
 Qy 481 YYEOTRGCGYIVCEPLPRGRQVQFCDAVTRGECHPWRGRGAALTVLGVDNEKDLDVAI 540
 Db 481 YYEOTRGCGYIVCEPLPRGRQVQFCDAVTRGECHPWRGRGAALTVLGVDNEKDLDVAI 540
 Qy 541 GAPEQENRGAVTLFHGASEGSPSHSQRIASQSLSPRLQYFGQALSGCQDLDQGLMD 600
 Db 541 GAPEQENRGAVTLFHGASEGSPSHSQRIASQSLSPRLQYFGQALSGCQDLDQGLMD 600
 Qy 601 LAVGARGOULLLSPLVPLKV3VAMRSPSVEVAKAVTRCWEKPSALBAGDATVCLTQKS 660
 Db 601 LAVGARGOULLLSPLVPLKV3VAMRSPSVEVAKAVTRCWEKPSALBAGDATVCLTQKS 660
 Qy 661 SLDLGDQSSVRFDLADPGRUTSRAIFNFTENINPTUTRKTGLTHCEIKLILLPDCV 720
 Db 661 SLDLGDQSSVRFDLADPGRUTSRAIFNFTENINPTUTRKTGLTHCEIKLILLPDCV 720
 Qy 721 EDVSPITLHNFSLVREPIPSQNLRVILAVGSQDFTASLPPENKGQGLCEGDLGV 780
 Db 721 EDVSPITLHNFSLVREPIPSQNLRVILAVGSQDFTASLPPENKGQGLCEGDLGV 780
 Qy 781 TLFSGLQTLTVGSSLEINNVITVWNAGSBDSTGTVVSDYYAAGLSSHRVSAQKQPHQSA 840
 Db 781 TLFSGLQTLTVGSSLEINNVITVWNAGSBDSTGTVVSDYYAAGLSSHRVSAQKQPHQSA 840
 Qy 841 LRLACETVETDEGLRSRCSVNHPIHEGSNTFTIVFDVSYKATLGDRMLMRASSE 900
 Db 841 LRLACETVETDEGLRSRCSVNHPIHEGSNTFTIVFDVSYKATLGDRMLMRASSE 900
 Qy 901 NNKASSKKATFOLELPVYCAVWVDMWMAPEQSLPCVSEKPPQHSDFTQIISSPMDCSIA 1020
 Db 901 NNKASSKKATFOLELPVYCAVWVDMWMAPEQSLPCVSEKPPQHSDFTQIISSPMDCSIA 1020
 Qy 961 DLAISINWVPPYLNGAVWVDMWMAPEQSLPCVSEKPPQHSDFTQIISSPMDCSIA 1020
 Db 961 DLAISINWVPPYLNGAVWVDMWMAPEQSLPCVSEKPPQHSDFTQIISSPMDCSIA 1020
 Qy 1021 DCLQFRCDVPSFSVQOBELDFTLKGNLNSFGWRETLOCKVLYVAELTDFDSVYSLPGQ 1080
 Db 1021 DCLQFRCDVPSFSVQOBELDFTLKGNLNSFGWRETLOCKVLYVAELTDFDSVYSLPGQ 1080
 Qy 1081 EAATRAQEMVLEEDDEVNAIPIMGSSVGAUILLALITATLYKLGFPKRYHEKMLEDCKP 1140
 Db 1081 EAATRAQEMVLEEDDEVNAIPIMGSSVGAUILLALITATLYKLGFPKRYHEKMLEDCKP 1140
 Qy 1141 EDATFSGDDFSCVAPNVPPLS 1161
 Db 1141 EDATFSGDDFSCVAPNVPPLS 1161

RESULT 2
 US-09-688-307A-2
 Sequence 2, Application US/09688307A

GENERAL INFORMATION:
 Patent No. 6432404
 APPLICANT: Galatin, Michael W.
 APPLICANT: Van der Vieren, Monica
 TITLE OF INVENTION: No. 6432404el Human Beta-2
 FILE REFERENCE: 27866/36646
 CURRENT APPLICATION NUMBER: US/09/688,307A
 CURRENT FILING DATE: 2000-10-13